```
1     cgagaaaaggtgacgcggggcccgggcaggcggccggcgcgcggcccccccccccccgc
61    cctggttatttggccgccttcgccggcagctcagggcagagtctcctggaaggcgcaggc
121   agtgtggcgagaagggcgcctgcttgttctttctttttgtctgctttcccccgtttgcgc
181   ctggaagctgcgccgcgagttcctgcaaggcggtctgccgcggccgggcccggccttctc
241   ccctcgcagcgaccccgcctcgcggccgcgcgggccccgaggtagcccgaggcgccggag
301   gagccagccccagcgagcgccgggagaggcggcagcgcagccggacgcacagcgcagcgg
361   gccggcaccagctcggccgggcccggactcggactcggcggccggcgcggcgcggcccgg
421   cccgagcgagggtgggggggcggcgggcggcgcgggg

457   cggcggcgagcgggggccATGCAGGCGCGCTACTCCGTGTCCAGCCCCAACTCC
      ..................METGlnAlaArgTyrSerValSerSerProAsnSer      12

511   CTGGGAGTGGTGCCCTACCTCGGCGGCGAGCAGAGCTACTACCGCGCGGCGGCC
      LeuGlyValValProTyrLeuGlyGlyGluGlnSerTyrTyrArgAlaAlaAla      30

565   GCGGCGGCCGGGGGCGGCTACACCGCCATGCCGGCCCCCATGAGCGTGTACTCG
      AlaAlaAlaGlyGlyGlyTyrThrAlaMETProAlaProMETSerValTyrSer      48

619   CACCCTGCGCACGCCGAGCAGTACCCGGGCGGCATGGCCCGCGCCTACGGGCCC
      HisProAlaHisAlaGluGlnTyrProGlyGlyMETAlaArgAlaTyrGlyPro      66

673   TACACGCCGCAGCCGCAGCCCAAGGACATGGTGAAGCCGCCCTATAGCTACATC
      TyrThrProGlnProGlnProLysAspMETValLysProProTyrSerTyrIle      84

727   GCGCTCATCACCATGGCCATCCAGAACGCCCCGGACAAGAAGATCACCCTGAAC
      AlaLeuIleThrMETAlaIleGlnAsnAlaProAspLysLysIleThrLeuAsn      102

781   GGCATCTACCAGTTCATCATGGACCGCTTCCCCTTCTACCGGGACAACAAGCAG
      GlyIleTyrGlnPheIleMETAspArgPheProPheTyrArgAspAsnLysGln      120

835   GGCTGGCAGAACAGCATCCGCCACAACCTCTCGCTCAACGAGTGCTTCGTCAAG
      GlyTrpGlnAsnSerIleArgHisAsnLeuSerLeuAsnGluCysPheValLys      138

889   GTGCCGCGCGACGACAAGAAGCCGGGCAAGGGCAGCTACTGGACGCTGGACCCG
      ValProArgAspAspLysLysProGlyLysGlySerTyrTrpThrLeuAspPro      156

943   GACTCCTACAACATGTTCGAGAACGGCAGCTTCCTGCGGCGGCGGCGGCGCTTC
      AspSerTryAsnMETPheGluAsnGlySerPheLeuArgArqArgArgArgPhe      174

997   AAGAAGAAGGACGCGGTGAAGGACAAGGAGGAGAAGGACAGGCTGCACCTCAAG
      LysLysLysAspAlaValLysAspLysGluGluLysAspArgLeuHisLeuLys      192

1051  GAGCCGCCCCCGCCCGGCCGCCAGCCCCCGCCCGCGCCGCCGGAGCAGGCCGAC
      GluProProProProGlyArgGlnProProProAlaProProGluGlnAlaAsp      210

1105  GGCAACGCGCCCGGTCCGCAGCCGCCGCCCGTGCGCATCCAGGACATCAAGACC
      GlyAsnAlaProGlyProGlnProProProValArgIleGlnAspIleLysThr      228

1159  GAGAACGGTACGTGCCCCTCGCCGCCCCAGCCCCTGTCCCCGGCCGCCGCCCTG
      GluAsnGlyThrCysProSerProProGlnProLeuSerProAlaAlaAlaLeu      246

1213  GGCAGCGGCAGCGCCGCCGCGGTGCCCAAGATCGAGAGCCCCGACAGCAGCAGC
      GlySerGlySerAlaAlaAlaValProLysIleGluSerProAspSerSerSer      264

1267  AGCAGCCTGTCCAGCGGGAGCAGCCCCCCGGGCAGCCTGCCGTCGGCGCGGCCG
      SerSerLeuSerSerGlySerSerProProGlySerLeuProSerAlaArgPro      282

1321  CTCAGCCTGGACGGTGCGGATTCCGCGCCGCCGCCGCCCGCGCCCTCCGCCCCG
      LeuSerLeuAspGlyAlaAspSerAlaProProProProAlaProSerAlaPro      300

1375  CCGCCGCACCATAGCCAGGGCTTCAGCGTGGACAACATCATGACGTCGCTGCGG
      ProProHisHisSerGlnGlyPheSerValAspAsnIleMETThrSerLeuArg      318

1429  GGGTCGCCGCAGAGCGCGGCCGCGGAGCTCAGCTCCGGCCTTCTGGCCTCGGCG
      GlySerProGlnSerAlaAlaAlaGluLeuSerSerGlyLeuLeuAlaSerAla      336

1483  GCCGCGTCCTCGCGCGCGGGGATCGCACCCCCGCTGGCGCTCGGCGCCTACTCG
      AlaAlaSerSerArgAlaGlyIleAlaProProLeuAlaLeuGlyAlaTyrSer      354

1537  CCCGGCCAGAGCTCCCTCTACAGCTCCCCCTGCAGCCAGACCTCCAGCGCGGGC
      ProGlyGlnSerSerLeuTyrSerSerProCysSerGlnThrSerSerAlaGly      372
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Fig. 1A

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1591  AGCTCGGGCGGCGGCGGCGGCGGCGCGGGGCCCGCGGGGGGCGCGGGCGGCGCC
      SerSerGlyGlyGlyGlyGlyGlyAlaGlyAlaAlaGlyGlyAlaGlyGlyAla      390

1645  GGGACCTACCACTGCAACCTGCAAGCCATGAGCCTGTACGCGGCCGGCGAGCGC
      GlyThrTyrHisCysAsnLeuGlnAlaMETSerLeuTyrAlaAlaGlyGluArg      408

1699  GGGGGCCACTTGCAGGGCGCGCCCGGGGGCGCGGGCGGCTCGGCCGTGGACAAC
      GlyGlyHisLeuGlnGlyAlaProGlyGlyAlaGlyGlySerAlaValAspAsn      426

1753  CCCCTGCCCGACTACTCTCTGCCTCCGGTCACCAGCAGCAGCTCGTCGTCCCTG
      ProLeuProAspTyrSerLeuProProValThrSerSerSerSerSerSerLeu      444

1807  AGTCACGGCGGCGGCGGCGGCGGCGGCGGGGGAGGCCAGGAGGCCGGCCACCAC
      SerHisGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlnGluAlaGlyHisHis      462

1861  CCTGCGGCCCACCAAGGCCGCCTCACCTCGTGGTACCTGAACCAGGCGGGCGGA
      ProAlaAlaHisGlnGlyArgLeuThrSerTrpTyrLeuAsnGlnAlaGlyGly      480

1915  GACCTGGGCCACTTGGCAAGCGCGGCGGCGGCGGCGGCGGCCGCAGGCTACCCG
      AspLeuGlyHisLeuAlaSerAlaAlaAlaAlaAlaAlaAlaAlaGlyTyrPro      498

1969  GGCCAGCAGCAGAACTTCCACTCGGTGCGGGAGATGTTCGAGTCACAGAGGATC
      GlyGlnGlnGlnAsnPheHisSerValArgGluMETPheGluSerGlnArgIle      516

2023  GGCTTGAACAACTCTCCAGTGAACGGGAATAGTAGCTGTCAAATGGCCTTCCCT
      GlyLeuAsnAsnSerProValAsnGlyAsnSerSerCysGlnMETAlaPhePro      534

2077  TCCAGCCAGTCTCTGTACCGCACGTCCGGAGCTTTCGTCTACGACTGTAGCAAG
      SerSerGlnSerLeuTyrArgThrSerGlyAlaPheValTyrAspCysSerLys      552

2131  TTTTGAcacaccctcaaagccgaactaaatcgaaccccaaagcaggaaaagcta
      PheSTP                                                      554


2185  aaggaacccatcaaggcaaaatcgaaactaaaaaaaaaaaatccaattaaaaaaaacccc
2245  tgagaatattcaccacaccagcgaacagaatatccctccaaaaattcagctcaccagcac
2305  cagcacgaagaaaactctattttcttaaccgattaattcagagccacctccactttgcct
2365  tgtctaaataaacaaacccgtaaactgttttatacagagacagcaaaatcttggtttatt
2425  aaaggacagtgttactccagataacacgtaagtttcttcttgcttttcagagacctgctt
2485  tcccctcctcccgtctcccctctcttgccttcttccttgcctctcacctgtaagatatta
2545  ttttatcctatgttgaagggaggggaaagtccccgtttatgaaagtcgctttcttttta
2605  ttcatggacttgttttaaaatgtaaattgcaacatagtaatttatttttaatttgtagtt
2665  ggatgtcgtggaccaaacgccagaaagtgttcccaaaacctgacgttaaattgcctgaaa
2725  ctttaaattgtgctttttttctcattataaaaagggaaactgtattaatcttattctatc
2785  ctcttttctttcttttgttgaacatattcattgtttgtttattaataaattaccattca
2845  qtttgaatgagacctatatgtctggatactttaatagagctttaattattacgaaaaaag
2905  atttcagagataaaacactagaagttacctattctccacctaaatctctgaaaaatggag
2965  aaaccctctgactagtccatgtcaaattttactaaaagtctttttgtttagatttatttt
3025  cctgcagcatcttctgcaaaatgtactatatagtcagcttgctttgaggctagtaaaaag
3085  atatttttctaaacagattggagttggcatataaacaaatacgttttctcactaatgaca
3145  gtccatgattcggaaatttaagcccatgaatcagccgcggtcttaccacggtgatgcct
3205  gtgtgccgagagatgggactgtgcggccagatatgcacagataaatatttggcttgtgta
3265  ttccatataaaattgcagtgcatattatacatccctgtgagccagatgctgaatagattt
3325  tttcctattatttcagtcctttataaaaggaaaaataaaccagttttaaatgtatgtat
3485  ataattctcccccatttacaatccttcatgtattacatagaaggattgctttttaaaaa
3445  tatactgcgggttggaaagggatatttaatctttgagaaactattttagaaaatatgttt
3505  gtagaacaattatttttgaaaaagatttaaagcaataacaagaaggaaggcgagaggagc
3565  agaacattttggtctagggtggtttctttttaaaccatttttttcttgttaatttacagtt
3625  aaacctaggggacaatccggattggccctcccccttttgtaaataacccaggaaatgtaa
3685  taaattcattatcttagggtgatctgccctgccaatcagactttggggagatggcgattt
3745  gattacagacgttcgggggggtgggggcttgcagtttgttttggagataatacagtttc
3805  ctgctatctgccgctcctatctagaggcaacacttaagcagtaattgctgttgcttgttg
3865  tcaaaatttgatcattgttaaaggattgctgcaaataaatacactttaatttcagtcaaa
3925  aaaaaaaaaaaaaaaaaaaaa
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Fig. 1B

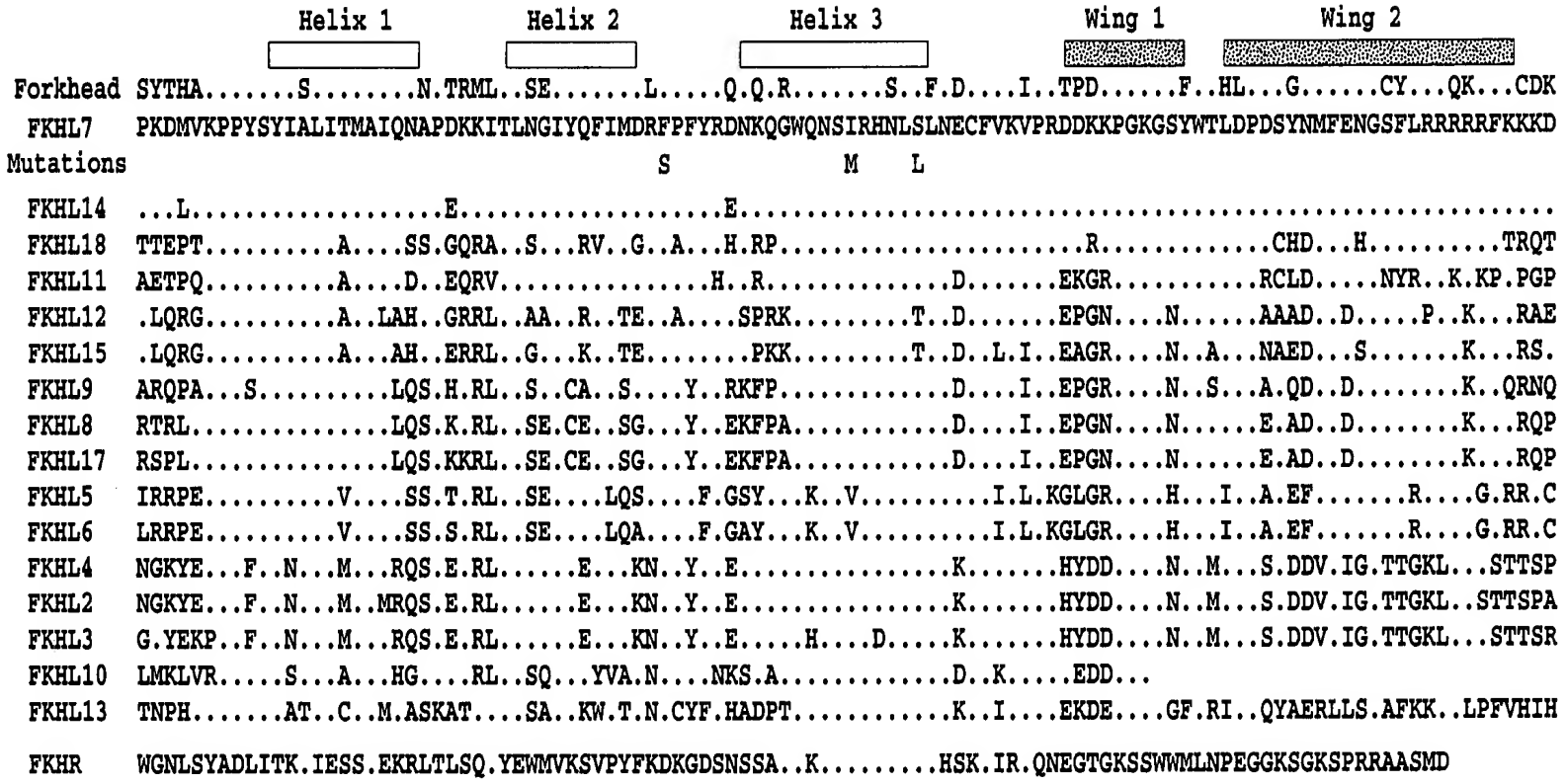

Fig. 2

Clone Name	Image Number	Organism	Vector	Loc	5' Sequence	3" Sequence	Insert Size	Tissue	Contig
zr45a08	666326	Human		3'	AA232742	AA232201		NhHMPu	
zw04a06	768274	Human		3'		AA424787		NhHMPu	
zv90g12	767110	Human		3'	AA424381	AA424466		NhHMPu	
yw76b12	258143	Human	pT7T3D	3'	N40575			Placenta, 8 to 9 wk	
ze13t07	358885	Human		3'		W94629		Fetal Heart	
yw78d12	258359	Human		3'		N25875		Placenta, 8 to 9 wk	
zw05a06	768370	Human	pT7T3D	3'	AA495846		722	NhHMPu	
oj36t08	1500423	Human		3'		AA885880		NCI_CGAP_Lu5	
zd71b11	346077	Human		3'	W77980			Fetal Heart, 19 wk	
ah14c11	1156628	Human		3'		AA776534		Wilms Tumor	
oh48b09	1469849	Human		3'		AA865139		NCI_CGAP_GC4	
zd71b12	346079	Human		3'		W73917		Fetal Heart, 19 wk	
ze71a01	364392	Human	pT7T3D	3'	AA022618	AA022755	919	Fetal Heart, 19 wk	
ze13t07	358885	Human		3'	W94714			Fetal Heart, 19 wk	
ok90g07	1521276	Human		3'		AA902429		NCI_CGAP_Lu5	
yw78b12	258335	Human		3'		N25867		Placenta, 8 to 9 wk	
yw28c11	253556	Human	pBlue SK-	3'	H89575			Fetal Cochlea	
EST54452		Human		3'	AA348051			Fetal Heart	
EST38957		Human		3'	AA334694			Embryo, 9 wk	
yw30d03	253733	Human	pBlue SK-	3'	N75774	N22552	475	Fetal Cochlea	
nj57a04	996558	Human		3'	AA551599			NCI_CGAP_Pr9	
yw76d12	258167	Human	pT7T3D	3'	N40582			Placenta, 8 to 9 wk	
nv16g07	1220412	Human		3'		AA688135		NCI_CGAP_Pr22	
GEN-206f07		Human		3'	D56550			Aorta	
oj39104	1500703	Human		3'		AA886687		NCI_CGAP_Kid3	
GEN-288A05		Human		3'	D57248			Aorta	
vc30a07	776052	Mouse	pT7T3D	3'	AA276025			Kidney, 6 wk	
vu08t03	1180061	Mouse		5'	AA673797			Myotubes	
vw64c01	1248576	Mouse		3'	AA960591	AA759405		Mammary Gland, 4 wk	
vg45c07	864300	Mouse	pT7T3D	3'		AA458089	936	Mammary Gland, 4 wk	
md53e12	372142	Mouse		3'		W57082		Embryo, 13.5-14.5 dy	
mt72a07	419796	Mouse	pT7T3D	5'	W91182			Embryo, 13.5-14.5 dy	
vv53d11	1226133	Mouse	pT7T3D	5'	AA739434			Thymus, 4 wk	
me94t07	403237	Mouse	pT7T3D	3'				Embryo, 13.5-14.5 dy	
vc85b07			pSPORT1	3'				Embryo, 11.5 dy	
mo83c06				3'					
UI-R-AO-al-b-03		Rat		3'	AA819240				
UI-R-E1-go-e-12		Rat		3'	AA964464			Embryo	

Fig. 3